

SEQUENCE LISTING

<110> MIYAWAKI, ATSUSHI
 KOGURE, TAKAKO
 HAMA, HIROSHI
 KINJO, MASATAKA
 SAITO, KENTA
 KARASAWA, SATOSHI
 ARAKI, TOSHIO

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<141> 2006-06-02

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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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 145 150 155 160
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 180 185 190
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 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
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 Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser	
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cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
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 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
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 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
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 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly	
20 25 30	
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc	144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala	
35 40 45	
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc	192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
50 55 60	
tgt tac ggc cac aga ggt ttt act aaa tat cca gaa gag ata cca gac	240
Cys Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp	
65 70 75 80	
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac	576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp	
180 185 190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
195 200 205	
gag ctg gta gaa gat gca gta gct cat tcc taa	657
Glu Leu Val Glu Asp Ala Val Ala His Ser	
210 215	

<210> 13

<211> 218

<212> PRT

<213> *Fungia* sp.

<400> 13

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Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25					30		
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
		35					40					45			
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
	50					55					60				
Cys	Tyr	Gly	His	Arg	Ala	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65					70					75					80
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85						90					95	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
			100					105					110		
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
		115					120					125			
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
	130					135					140				
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145					150					155					160
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
				165					170					175	
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
			180					185					190		
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr
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Glu	Leu	Val	Glu	Asp	Ala	Val	Ala	His	Ser						
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<210> 14

<211> 657

<212> DNA

<213> Fungia sp.

<220>

<221> CDS

<222> (1)..(654)

<400> 14

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1				5					10					15		

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

tgt	tac	ggc	cac	aga	gct	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240
Cys	Tyr	Gly	His	Arg	Ala	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
65					70					75					80	

tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	tca	tgg	gaa	agg	tcg	ttg	288
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
				85					90					95		

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
115 120 125

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140

tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	gtt	ctg	aag	ggt	gat	gtt	480
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	
145					150					155					160	

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
165 170 175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190

cat tac atc ggg cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215

<210> 15
 <211> 218
 <212> PRT
 <213> Fungia sp.

<400> 15

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Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25					30		
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
		35					40					45			
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
	50					55					60				
Cys	Tyr	Gly	His	Arg	Ser	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65					70					75					80
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
				85					90					95	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
			100					105					110		
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
		115					120					125			
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
	130					135					140				
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145					150					155					160
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
				165					170					175	
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
			180					185					190		
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr
		195					200					205			
Glu	Leu	Val	Glu	Asp	Ala	Val	Ala	His	Ser						
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<210> 16
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 <212> DNA
 <213> Fungia sp.

<220>

<221> CDS

<222> (1) .. (654)

<400> 16

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1				5					10					15		
ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	gaa	ggg	gaa	ggc	aca	ggc	96
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	
			20					25						30		
aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	cta	cgc	gtc	aca	atg	gcc	144
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
		35					40					45				
gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
	50					55					60					
tgt	tac	ggc	cac	aga	tct	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240
Cys	Tyr	Gly	His	Arg	Ser	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
65					70				75						80	
tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	tca	tgg	gaa	agg	tcg	ttg	288
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
			85						90					95		
gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	
			100					105					110			
aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	ttt	act	ggg	gtt	aac	ttt	384
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	
		115					120					125				
cct	gcc	gat	ggg	cct	atc	atg	caa	aac	caa	agt	gtt	gat	tgg	gag	cca	432
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	
	130					135					140					
tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	gtt	ctg	aag	ggg	gat	gtt	480
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	
145					150					155					160	
acg	atg	tac	cta	aaa	ctt	gaa	gga	ggc	ggc	aat	cac	aaa	tgc	caa	ttc	528
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe	
				165					170					175		
aag	act	act	tac	aag	gcg	gca	aaa	gag	att	ctt	gaa	atg	cca	gga	gac	576
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp	
			180					185					190			
cat	tac	atc	ggc	cat	cgc	ctc	gtc	agg	aaa	acc	gaa	ggc	aac	att	act	624
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr	
		195					200					205				

gag ctg gta gaa gat gca gta gct cat tcc taa
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

657

<210> 17
 <211> 218
 <212> PRT
 <213> *Fungia* sp.

<400> 17
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 18
 <211> 657
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 <213> *Fungia* sp.

<220>
 <221> CDS
 <222> (1)..(654)

<400> 18

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1				5					10					15		
ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	gaa	ggg	gaa	ggc	aca	ggc	96
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	
			20					25					30			
aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	cta	cgc	gtc	aca	atg	gcc	144
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
		35					40					45				
gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
	50					55					60					
tgt	tac	ggc	cac	aga	tgt	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240
Cys	Tyr	Gly	His	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
65					70				75						80	
tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	tca	tgg	gaa	agg	tcg	ttg	288
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
			85						90					95		
gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	
			100					105					110			
aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	ttt	act	ggg	gtt	aac	ttt	384
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	
		115					120					125				
cct	gcc	gat	ggg	cct	atc	atg	caa	aac	caa	agt	gtt	gat	tgg	gag	cca	432
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	
	130					135					140					
tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	gtt	ctg	aag	ggg	gat	gtt	480
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	
145					150					155					160	
acg	atg	tac	cta	aaa	ctt	gaa	gga	ggc	ggc	aat	cac	aaa	tgc	caa	ttc	528
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe	
				165				170						175		
aag	act	act	tac	aag	gcg	gca	aaa	gag	att	ctt	gaa	atg	cca	gga	gac	576
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp	
			180					185					190			

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 19
 <211> 218
 <212> PRT
 <213> Fungia sp.

<400> 19
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 Cys Tyr Gly His Arg Thr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 20
 <211> 657
 <212> DNA
 <213> *Fungia* sp.

<220>
 <221> CDS
 <222> (1)..(654)

<400> 20

atg	gtg	agt	gtg	att	aaa	cca	gag	atg	aag	atg	agg	tac	tac	atg	gac	48
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ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	gaa	ggg	gaa	ggc	aca	ggc	96
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	
			20					25					30			
aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	cta	cgc	gtc	aca	atg	gcc	144
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	
		35					40					45				
gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	tta	gtg	tca	cac	gtg	ttc	192
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	
	50					55					60					
tgt	tac	ggc	cac	aga	act	ttt	act	aaa	tat	cca	gaa	gag	ata	cca	gac	240
Cys	Tyr	Gly	His	Arg	Thr	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
65					70					75					80	
tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	tca	tgg	gaa	agg	tcg	ttg	288
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	
			85						90					95		
gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	agt	gcg	cat	ata	agc	ctt	336
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	
			100					105					110			
aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	ttt	act	ggg	gtt	aac	ttt	384
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	
		115					120					125				
cct	gcc	gat	ggg	cct	atc	atg	caa	aac	caa	agt	gtt	gat	tgg	gag	cca	432
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	
	130					135					140					
tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	gtt	ctg	aag	ggg	gat	gtt	480
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	
145					150					155					160	
acg	atg	tac	cta	aaa	ctt	gaa	gga	ggc	ggc	aat	cac	aaa	tgc	caa	ttc	528
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe	
				165				170						175		
aag	act	act	tac	aag	gcg	gca	aaa	gag	att	ctt	gaa	atg	cca	gga	gac	576
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp	
			180					185					190			

<210> 22
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 <213> *Fungia* sp.

<220>
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<400> 22

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac	48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp	
1 5 10 15	
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc	96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly	
20 25 30	
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc	144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala	
35 40 45	
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc	192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
50 55 60	
tgt tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac	240
Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp	
65 70 75 80	
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 23

<211> 218

<212> PRT

<213> *Fungia* sp.

<400> 23

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 24
 <211> 657
 <212> DNA
 <213> *Fungia* sp.

<220>
 <221> CDS
 <222> (1) .. (654)

<400> 24
 atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

tgt tac ggc cac aga ctt ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 25
 <211> 218
 <212> PRT
 <213> Fungia sp.

<400> 25
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 26
 <211> 657
 <212> DNA
 <213> Fungia sp.

<220>
 <221> CDS
 <222> (1)..(654)

<400> 26
 atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

tgt tac ggc cac aga tac ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

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tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145                      150                      155                      160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
                      165                      170                      175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
                      180                      185                      190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
                      195                      200                      205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
210                      215

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<210> 27
<211> 218
<212> PRT
<213> Fungia sp.

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<400> 27
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1                      5                      10                      15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
                20                      25                      30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
    35                      40                      45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
    50                      55                      60

Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
    65                      70                      75                      80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
    85                      90                      95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
    100                      105                      110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
    115                      120                      125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
    130                      135                      140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
    145                      150                      155                      160

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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 28
 <211> 657
 <212> DNA
 <213> Fungia sp.

<220>
 <221> CDS
 <222> (1)..(654)

<400> 28
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 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

tgt tac ggc cac aga cag ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

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cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
130 135 140

tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
165 170 175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
180 185 190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa 657
Glu Leu Val Glu Asp Ala Val Ala His Ser
210 215

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<210> 29
 <211> 218
 <212> PRT
 <213> *Fungia* sp.

<220>
 <221> MOD_RES
 <222> (186)
 <223> variable amino acid

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<400> 29
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
1 5 10 15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60

Cys Tyr Gly His Arg Asn Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
100 105 110

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Xaa Leu Glu Met Pro Gly Asp
 180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 30
 <211> 657
 <212> DNA
 <213> Fungia sp.

<220>
 <221> CDS
 <222> (1)..(654)

<220>
 <221> modified_base
 <222> (556)
 <223> a, c, g, t, unknown or other

<400> 30
 atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
 1 5 10 15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60

tgt tac ggc cac aga aat ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Asn Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	
aag act act tac aag gcg gca aaa gag ntt ctt gaa atg cca gga gac	576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Xaa Leu Glu Met Pro Gly Asp	
180 185 190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
195 200 205	
gag ctg gta gaa gat gca gta gct cat tcc taa	657
Glu Leu Val Glu Asp Ala Val Ala His Ser	
210 215	

<210> 31
 <211> 665
 <212> PRT
 <213> *Fungia* sp.

<400> 31
 Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
 1 5 10 15
 Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
 20 25 30
 Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
 35 40 45
 Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
 50 55 60
 Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
 65 70 75 80

Asp	Glu	Gly	Ala	Pro	Gly	Lys	Gln	Ala	Ala	Ala	Gln	Pro	His	Thr	Glu	
				85					90					95		
Ile	Pro	Glu	Gly	Thr	Thr	Ala	Glu	Glu	Ala	Gly	Ile	Gly	Asp	Thr	Pro	
			100					105					110			
Ser	Leu	Glu	Asp	Glu	Ala	Ala	Gly	His	Val	Thr	Gln	Ala	Arg	Met	Val	
		115					120					125				
Ser	Lys	Ser	Lys	Asp	Gly	Thr	Gly	Ser	Asp	Asp	Lys	Lys	Ala	Lys	Gly	
	130					135					140					
Ala	Asp	Gly	Lys	Thr	Lys	Ile	Ala	Thr	Pro	Arg	Gly	Ala	Ala	Pro	Pro	
145					150					155					160	
Gly	Gln	Lys	Gly	Gln	Ala	Asn	Ala	Thr	Arg	Ile	Pro	Ala	Lys	Thr	Pro	
				165					170					175		
Pro	Ala	Pro	Lys	Thr	Pro	Pro	Ser	Ser	Gly	Glu	Pro	Pro	Lys	Ser	Gly	
			180					185					190			
Asp	Arg	Ser	Gly	Tyr	Ser	Ser	Pro	Gly	Ser	Pro	Gly	Thr	Pro	Gly	Ser	
		195					200					205				
Arg	Ser	Arg	Thr	Pro	Ser	Leu	Pro	Thr	Pro	Pro	Thr	Arg	Glu	Pro	Lys	
	210					215					220					
Lys	Val	Ala	Val	Val	Arg	Thr	Pro	Pro	Lys	Ser	Pro	Ser	Ser	Ala	Lys	
225					230					235					240	
Ser	Arg	Leu	Gln	Thr	Ala	Pro	Val	Pro	Met	Pro	Asp	Leu	Lys	Asn	Val	
			245						250					255		
Lys	Ser	Lys	Ile	Gly	Ser	Thr	Glu	Asn	Leu	Lys	His	Gln	Pro	Gly	Gly	
			260					265					270			
Gly	Lys	Val	Gln	Ile	Ile	Asn	Lys	Lys	Leu	Asp	Leu	Ser	Asn	Val	Gln	
		275					280					285				
Ser	Lys	Cys	Gly	Ser	Lys	Asp	Asn	Ile	Lys	His	Val	Pro	Gly	Gly	Gly	
	290					295					300					
Ser	Val	Gln	Ile	Val	Tyr	Lys	Pro	Val	Asp	Leu	Ser	Lys	Val	Thr	Ser	
305					310					315					320	
Lys	Cys	Gly	Ser	Leu	Gly	Asn	Ile	His	His	Lys	Pro	Gly	Gly	Gly	Gln	
			325						330					335		
Val	Glu	Val	Lys	Ser	Glu	Lys	Leu	Asp	Phe	Lys	Asp	Arg	Val	Gln	Ser	
			340					345					350			
Lys	Ile	Gly	Ser	Leu	Asp	Asn	Ile	Thr	His	Val	Pro	Gly	Gly	Gly	Asn	
	355						360					365				
Lys	Lys	Ile	Glu	Thr	His	Lys	Leu	Thr	Phe	Arg	Glu	Asn	Ala	Lys	Ala	
	370					375					380					

Lys	Thr	Asp	His	Gly	Ala	Glu	Ile	Val	Tyr	Lys	Ser	Pro	Val	Val	Ser	385	390	395	400
Gly	Asp	Thr	Ser	Pro	Arg	His	Leu	Ser	Asn	Val	Ser	Ser	Thr	Gly	Ser	405	410	415	
Ile	Asp	Met	Val	Asp	Ser	Pro	Gln	Leu	Ala	Thr	Leu	Ala	Asp	Glu	Val	420	425	430	
Ser	Ala	Ser	Leu	Ala	Lys	Gln	Gly	Leu	Gly	Ser	Gly	Gly	Glu	Phe	Met	435	440	445	
Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp	Gly	450	455	460	
Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly	Arg	465	470	475	480
Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala	Glu	485	490	495	
Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe	Cys	500	505	510	
Tyr	Gly	His	Arg	Val	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	Tyr	515	520	525	
Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu	Glu	530	535	540	
Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu	Arg	545	550	555	560
Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe	Pro	565	570	575	
Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro	Ser	580	585	590	
Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	Thr	595	600	605	
Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe	Lys	610	615	620	
Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp	His	625	630	635	640
Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr	Glu	645	650	655	
Leu	Val	Glu	Asp	Ala	Val	Ala	His	Ser								660	665		

<210> 32
 <211> 1998
 <212> DNA
 <213> *Fungia* sp.

<220>
 <221> CDS
 <222> (1)..(1995)

<400> 32

atg gct gag ccc cgc cag gag ttc gaa gtg atg gaa gat cac gct ggg	48
Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly	
1 5 10 15	
acg tac ggg ttg ggg gac agg aaa gat cag ggg ggc tac acc atg cac	96
Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His	
20 25 30	
caa gac caa gag ggt gac acg gac gct ggc ctg aaa gaa tct ccc ctg	144
Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu	
35 40 45	
cag acc ccc act gag gac gga tct gag gaa ccg ggc tct gaa acc tct	192
Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser	
50 55 60	
gat gct aag agc act cca aca gcg gaa gat gtg aca gca ccc tta gtg	240
Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val	
65 70 75 80	
gat gag gga gct ccc ggc aag cag gct gcc gcg cag ccc cac acg gag	288
Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu	
85 90 95	
atc cca gaa gga acc aca gct gaa gaa gca ggc att gga gac acc ccc	336
Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro	
100 105 110	
agc ctg gaa gac gaa gct gct ggt cac gtg acc caa gct cgc atg gtc	384
Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val	
115 120 125	
agt aaa agc aaa gac ggg act gga agc gat gac aaa aaa gcc aag ggg	432
Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly	
130 135 140	
gct gat ggt aaa acg aag atc gcc aca ccg cgg gga gca gcc cct cca	480
Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro	
145 150 155 160	
ggc cag aag ggc cag gcc aac gcc acc agg att cca gca aaa acc ccg	528
Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro	
165 170 175	
ccc gct cca aag aca cca ccc agc tct ggt gaa cct cca aaa tca ggg	576
Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly	
180 185 190	

gat	cgc	agc	ggc	tac	agc	agc	ccc	ggc	tcc	cca	ggc	act	ccc	ggc	agc	624
Asp	Arg	Ser	Gly	Tyr	Ser	Ser	Pro	Gly	Ser	Pro	Gly	Thr	Pro	Gly	Ser	
		195					200					205				
cgc	tcc	cgc	acc	ccg	tcc	ctt	cca	acc	cca	ccc	acc	cgg	gag	ccc	aag	672
Arg	Ser	Arg	Thr	Pro	Ser	Leu	Pro	Thr	Pro	Pro	Thr	Arg	Glu	Pro	Lys	
	210					215					220					
aag	gtg	gca	gtg	gtc	cgt	act	cca	ccc	aag	tcg	ccg	tct	tcc	gcc	aag	720
Lys	Val	Ala	Val	Val	Arg	Thr	Pro	Pro	Lys	Ser	Pro	Ser	Ser	Ala	Lys	
225					230				235						240	
agc	cgc	ctg	cag	aca	gcc	ccc	gtg	ccc	atg	cca	gac	ctg	aag	aat	gtc	768
Ser	Arg	Leu	Gln	Thr	Ala	Pro	Val	Pro	Met	Pro	Asp	Leu	Lys	Asn	Val	
			245						250					255		
aag	tcc	aag	atc	ggc	tcc	act	gag	aac	ctg	aag	cac	cag	ccg	gga	ggc	816
Lys	Ser	Lys	Ile	Gly	Ser	Thr	Glu	Asn	Leu	Lys	His	Gln	Pro	Gly	Gly	
			260					265					270			
ggg	aag	gtg	cag	ata	att	aat	aag	aag	ctg	gat	ctt	agc	aac	gtc	cag	864
Gly	Lys	Val	Gln	Ile	Ile	Asn	Lys	Lys	Leu	Asp	Leu	Ser	Asn	Val	Gln	
		275					280					285				
tcc	aag	tgt	ggc	tca	aag	gat	aat	atc	aaa	cac	gtc	ccg	gga	ggc	ggc	912
Ser	Lys	Cys	Gly	Ser	Lys	Asp	Asn	Ile	Lys	His	Val	Pro	Gly	Gly	Gly	
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agt	gtg	caa	ata	gtc	tac	aaa	cca	gtt	gac	ctg	agc	aag	gtg	acc	tcc	960
Ser	Val	Gln	Ile	Val	Tyr	Lys	Pro	Val	Asp	Leu	Ser	Lys	Val	Thr	Ser	
305					310					315					320	
aag	tgt	ggc	tca	tta	ggc	aac	atc	cat	cat	aaa	cca	gga	ggt	ggc	cag	1008
Lys	Cys	Gly	Ser	Leu	Gly	Asn	Ile	His	His	Lys	Pro	Gly	Gly	Gly	Gln	
			325						330					335		
gtg	gaa	gta	aaa	tct	gag	aag	ctt	gac	ttc	aag	gac	aga	gtc	cag	tcg	1056
Val	Glu	Val	Lys	Ser	Glu	Lys	Leu	Asp	Phe	Lys	Asp	Arg	Val	Gln	Ser	
			340					345					350			
aag	att	ggg	tcc	ctg	gac	aat	atc	acc	cac	gtc	cct	ggc	gga	gga	aat	1104
Lys	Ile	Gly	Ser	Leu	Asp	Asn	Ile	Thr	His	Val	Pro	Gly	Gly	Gly	Asn	
		355					360					365				
aaa	aag	att	gaa	acc	cac	aag	ctg	acc	ttc	cgc	gag	aac	gcc	aaa	gcc	1152
Lys	Lys	Ile	Glu	Thr	His	Lys	Leu	Thr	Phe	Arg	Glu	Asn	Ala	Lys	Ala	
	370					375					380					
aag	aca	gac	cac	ggg	gcg	gag	atc	gtg	tac	aag	tcg	cca	gtg	gtg	tct	1200
Lys	Thr	Asp	His	Gly	Ala	Glu	Ile	Val	Tyr	Lys	Ser	Pro	Val	Val	Ser	
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ggg	gac	acg	tct	cca	cgg	cat	ctc	agc	aat	gtc	tcc	tcc	acc	ggc	agc	1248
Gly	Asp	Thr	Ser	Pro	Arg	His	Leu	Ser	Asn	Val	Ser	Ser	Thr	Gly	Ser	
				405					410					415		

atc gac atg gta gac tcg ccc cag ctc gcc acg cta gct gac gag gtg	1296
Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val	
420 425 430	
tct gcc tcc ctg gcc aag cag ggt ttg gga tcc gga ggt gaa ttc atg	1344
Ser Ala Ser Leu Ala Lys Gln Gly Leu Gly Ser Gly Gly Glu Phe Met	
435 440 445	
gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac ggc	1392
Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp Gly	
450 455 460	
tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc aga	1440
Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly Arg	
465 470 475 480	
cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc gag	1488
Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala Glu	
485 490 495	
ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc tgt	1536
Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe Cys	
500 505 510	
tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac tat	1584
Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp Tyr	
515 520 525	
ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg gag	1632
Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu Glu	
530 535 540	
ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt aga	1680
Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu Arg	
545 550 555 560	
gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt cct	1728
Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe Pro	
565 570 575	
gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca tca	1776
Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro Ser	
580 585 590	
acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt acg	1824
Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val Thr	
595 600 605	
atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc aag	1872
Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe Lys	
610 615 620	
act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac cat	1920
Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp His	
625 630 635 640	

tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act gag 1968
 Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr Glu
 645 650 655

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 Leu Val Glu Asp Ala Val Ala His Ser
 660 665

<210> 33
 <211> 480
 <212> PRT
 <213> Fungia sp.

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 20 25 30
 Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn
 35 40 45
 Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp
 50 55 60
 Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val
 65 70 75 80
 Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg
 85 90 95
 Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu
 100 105 110
 Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg
 115 120 125
 Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys
 130 135 140
 Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val
 145 150 155 160
 Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser
 165 170 175
 Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met
 180 185 190
 Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn
 195 200 205
 Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp
 210 215 220

Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys
 225 230 235 240
 Val Cys Thr Leu Thr Ile Lys Arg Gly Arg Gly Val Pro Arg Ala Arg
 245 250 255
 Asp Pro Pro Val Ala Thr Met Val Ser Val Ile Lys Pro Glu Met Lys
 260 265 270
 Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
 275 280 285
 Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
 290 295 300
 Leu Arg Val Thr Met Ala Glu Gly Gly Pro Met Pro Phe Ala Phe Asp
 305 310 315 320
 Leu Val Ser His Val Phe Cys Tyr Gly His Arg Val Phe Thr Lys Tyr
 325 330 335
 Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
 340 345 350
 Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val
 355 360 365
 Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys
 370 375 380
 Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln
 385 390 395 400
 Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
 405 410 415
 Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
 420 425 430
 Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile
 435 440 445
 Leu Glu Met Pro Gly Asp His Tyr Ile Gly His Arg Leu Val Arg Lys
 450 455 460
 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
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<210> 34

<211> 1443

<212> DNA

<213> Fungia sp.

<220>

<221> CDS

<222> (1)..(1440)

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atg aag gct gcg ccc atg aaa gaa gca aac gtc cac gga caa ggc aac	96
Met Lys Ala Ala Pro Met Lys Glu Ala Asn Val His Gly Gln Gly Asn	
20 25 30	
ttg gcc tac cca gct gtg cgg acc cat ggg act ctg gag agc gtg aat	144
Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn	
35 40 45	
ggg ccc agg gca ggt tcg aga ggt ctg acg acg acg tcc ctg gct gac	192
Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp	
50 55 60	
act ttt gag cac gtg atc gaa gag ctg ctg gat gag gac cag aag gtt	240
Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val	
65 70 75 80	
cgg ccc aac gaa gaa aac cat aag gac gcg gac ttg tac act tcc cgg	288
Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg	
85 90 95	
gtg atg ctc agc agt caa gtg cct ttg gag cct cct ctg ctc ttt ctg	336
Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu	
100 105 110	
ctg gag gaa tac aaa aat tac ctg gat gcc gca aac atg tct atg agg	384
Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg	
115 120 125	
gtt cgg cgc cac tcc gac ccc gcc cgc cgt ggg gag ctg agc gtg tgt	432
Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys	
130 135 140	
gac agt att agc gag tgg gtc aca gcg gca gat aaa aag act gca gtg	480
Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val	
145 150 155 160	
gac atg tcc ggt ggg acg gtc aca gtc ctg gag aaa gtc ccg gta tca	528
Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser	
165 170 175	
aaa ggc caa ctg aag caa tat ttc tac gag acc aag tgt aat ccc atg	576
Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met	
180 185 190	
ggt tac acg aag gaa ggc tgc agg ggc ata gac aaa agg cac tgg aac	624
Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn	
195 200 205	

tcg	caa	tgc	cga	act	acc	caa	tcg	tat	gtt	cgg	gcc	ctt	act	atg	gat	672
Ser	Gln	Cys	Arg	Thr	Thr	Gln	Ser	Tyr	Val	Arg	Ala	Leu	Thr	Met	Asp	
	210						215				220					
agc	aaa	aag	aga	att	ggc	tgg	cgg	ttc	ata	agg	ata	gac	act	tcc	tgt	720
Ser	Lys	Lys	Arg	Ile	Gly	Trp	Arg	Phe	Ile	Arg	Ile	Asp	Thr	Ser	Cys	
	225				230					235					240	
gta	tgt	aca	ctg	acc	att	aaa	agg	gga	aga	ggg	gta	ccg	cgg	gcc	cgg	768
Val	Cys	Thr	Leu	Thr	Ile	Lys	Arg	Gly	Arg	Gly	Val	Pro	Arg	Ala	Arg	
				245					250					255		
gac	cca	ccg	gtc	gcc	acc	atg	gtg	agt	gtg	att	aaa	cca	gag	atg	aag	816
Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	
			260					265					270			
atg	agg	tac	tac	atg	gac	ggc	tcc	gtc	aat	ggg	cat	gag	ttc	aca	att	864
Met	Arg	Tyr	Tyr	Met	Asp	Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	
		275					280					285				
gaa	ggg	gaa	ggc	aca	ggc	aga	cct	tac	gag	gga	cat	caa	gag	atg	aca	912
Glu	Gly	Glu	Gly	Thr	Gly	Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	
	290					295					300					
cta	cgc	gtc	aca	atg	gcc	gag	ggc	ggg	cca	atg	cct	ttc	gcg	ttt	gac	960
Leu	Arg	Val	Thr	Met	Ala	Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	
	305				310					315					320	
tta	gtg	tca	cac	gtg	ttc	tgt	tac	ggc	cac	aga	gta	ttt	act	aaa	tat	1008
Leu	Val	Ser	His	Val	Phe	Cys	Tyr	Gly	His	Arg	Val	Phe	Thr	Lys	Tyr	
				325					330					335		
cca	gaa	gag	ata	cca	gac	tat	ttc	aaa	caa	gca	ttt	cct	gaa	ggc	ctg	1056
Pro	Glu	Glu	Ile	Pro	Asp	Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	
			340					345					350			
tca	tgg	gaa	agg	tcg	ttg	gag	ttc	gaa	gat	ggg	ggg	tcc	gct	tca	gtc	1104
Ser	Trp	Glu	Arg	Ser	Leu	Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	
		355					360					365				
agt	gcg	cat	ata	agc	ctt	aga	gga	aac	acc	ttc	tac	cac	aaa	tcc	aaa	1152
Ser	Ala	His	Ile	Ser	Leu	Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	
	370					375					380					
ttt	act	ggg	gtt	aac	ttt	cct	gcc	gat	ggg	cct	atc	atg	caa	aac	caa	1200
Phe	Thr	Gly	Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	
	385				390					395					400	
agt	gtt	gat	tgg	gag	cca	tca	acc	gag	aaa	att	act	gcc	agc	gac	gga	1248
Ser	Val	Asp	Trp	Glu	Pro	Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	
				405					410					415		
gtt	ctg	aag	ggg	gat	gtt	acg	atg	tac	cta	aaa	ctt	gaa	gga	ggc	ggc	1296
Val	Leu	Lys	Gly	Asp	Val	Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	
			420					425						430		

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aat cac aaa tgc caa ttc aag act act tac aag gcg gca aaa gag att 1344
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile
      435                      440                      445

ctt gaa atg cca gga gac cat tac atc ggc cat cgc ctc gtc agg aaa 1392
Leu Glu Met Pro Gly Asp His Tyr Ile Gly His Arg Leu Val Arg Lys
      450                      455                      460

acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1440
Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
      465                      470                      475                      480

taa 1443

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<210> 35
<211> 464
<212> PRT
<213> Fungia sp.

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Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly
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Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val
      35              40              45

Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
      50              55              60

Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
      65              70              75              80

Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
      85              90              95

Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
      100             105             110

Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
      115             120             125

Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
      130             135             140

Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
      145             150             155             160

Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln
      165             170             175

Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
      180             185             190

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Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
 195 200 205
 Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala
 210 215 220
 His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val
 225 230 235 240
 Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys
 245 250 255
 Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
 260 265 270
 Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
 275 280 285
 Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp
 290 295 300
 Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr
 305 310 315 320
 Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
 325 330 335
 Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val
 340 345 350
 Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys
 355 360 365
 Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln
 370 375 380
 Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
 385 390 395 400
 Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
 405 410 415
 Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile
 420 425 430
 Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys
 435 440 445
 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
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<210> 36

<211> 1395

<212> DNA

<213> *Fungia* sp.

<220>

<221> CDS

<222> (1)..(1392)

<400> 36

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1				5					10					15		
tac	cgt	atg	gaa	ggc	agt	gtc	aat	ggc	cat	gaa	ttc	acg	atc	gaa	ggc	96
Tyr	Arg	Met	Glu	Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	
			20					25					30			
gta	gga	act	gga	aac	cct	tac	gaa	ggg	aaa	cag	atg	tcc	gaa	tta	gtg	144
Val	Gly	Thr	Gly	Asn	Pro	Tyr	Glu	Gly	Lys	Gln	Met	Ser	Glu	Leu	Val	
			35					40				45				
atc	atc	aag	tct	aag	gga	aaa	ccc	ctt	cca	ttc	tcc	ttt	gac	ata	ctg	192
Ile	Ile	Lys	Ser	Lys	Gly	Lys	Pro	Leu	Pro	Phe	Ser	Phe	Asp	Ile	Leu	
		50				55						60				
tca	aca	gcc	ttt	caa	tat	gga	aac	aga	tgc	ttc	aca	aag	tac	cct	gca	240
Ser	Thr	Ala	Phe	Gln	Tyr	Gly	Asn	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Ala	
	65					70				75					80	
gac	atg	cct	gac	tat	ttc	aag	caa	gca	ttc	cca	gat	gga	atg	tca	tat	288
Asp	Met	Pro	Asp	Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Asp	Gly	Met	Ser	Tyr	
				85					90					95		
gaa	agg	tca	ttt	cta	ttt	gag	gat	gga	gga	gtt	gct	aca	gcc	agc	tgg	336
Glu	Arg	Ser	Phe	Leu	Phe	Glu	Asp	Gly	Gly	Val	Ala	Thr	Ala	Ser	Trp	
			100					105					110			
agc	att	cgt	ctc	gaa	gga	aat	tgc	ttc	atc	cac	aat	tcc	atc	tat	cat	384
Ser	Ile	Arg	Leu	Glu	Gly	Asn	Cys	Phe	Ile	His	Asn	Ser	Ile	Tyr	His	
		115					120					125				
ggc	gta	aac	ttt	ccc	gct	gat	gga	ccc	gta	atg	aag	aag	cag	aca	att	432
Gly	Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Gln	Thr	Ile	
	130					135					140					
ggc	tgg	gat	aag	tcc	ttc	gaa	aaa	atg	agt	gtg	gct	aaa	gag	gtg	cta	480
Gly	Trp	Asp	Lys	Ser	Phe	Glu	Lys	Met	Ser	Val	Ala	Lys	Glu	Val	Leu	
145.					150					155				160		
aga	ggc	gat	gtg	act	cag	ttt	ctt	ctg	ctc	gaa	gga	ggc	ggc	tac	cag	528
Arg	Gly	Asp	Val	Thr	Gln	Phe	Leu	Leu	Leu	Glu	Gly	Gly	Gly	Tyr	Gln	
				165					170					175		
aga	tgc	cgg	ttt	cac	tcc	act	tac	aaa	acg	gag	aag	cca	gtc	gca	atg	576
Arg	Cys	Arg	Phe	His	Ser	Thr	Tyr	Lys	Thr	Glu	Lys	Pro	Val	Ala	Met	
			180					185					190			
ccc	ccg	agt	cat	gtc	gta	gaa	cat	caa	att	gtg	agg	acc	gac	ctt	ggc	624
Pro	Pro	Ser	His	Val	Val	Glu	His	Gln	Ile	Val	Arg	Thr	Asp	Leu	Gly	
		195					200					205				

caa Gln	act Thr	gca Ala	aaa Lys	ggc Gly	ttc Phe	aag Lys	gtc Val	aag Lys	ctg Leu	gaa Glu	gaa Glu	cat His	gct Ala	gag Glu	gct Ala	672
210						215				220						
cat His	gtt Val	aac Asn	cct Pro	ttg Leu	aag Lys	gtt Val	aaa Lys	ggg Gly	ggc Gly	agc Ser	ggg Gly	ggc Gly	gac Asp	gag Glu	gtg Val	720
225					230					235					240	
gac Asp	ggg Gly	acc Thr	ggg Gly	ggc Gly	agc Ser	atg Met	gtg Val	agt Ser	gtg Val	att Ile	aaa Lys	cca Pro	gag Glu	atg Met	aag Lys	768
				245					250					255		
atg Met	agg Arg	tac Tyr	tac Tyr	atg Met	gac Asp	ggc Gly	tcc Ser	gtc Val	aat Asn	ggg Gly	cat His	gag Glu	ttc Phe	aca Thr	att Ile	816
			260					265					270			
gaa Glu	ggg Gly	gaa Glu	ggc Gly	aca Thr	ggc Gly	aga Arg	cct Pro	tac Tyr	gag Glu	gga Gly	cat His	caa Gln	gag Glu	atg Met	aca Thr	864
	275						280					285				
cta Leu	cgc Arg	gtc Val	aca Thr	atg Met	gcc Ala	aag Lys	ggc Gly	ggg Gly	cca Pro	atg Met	cct Pro	ttc Phe	gcg Ala	ttt Phe	gac Asp	912
	290					295					300					
tta Leu	gtg Val	tca Ser	cac His	gtg Val	ttc Phe	tgt Cys	tac Tyr	ggc Gly	cac His	aga Arg	cct Pro	ttt Phe	act Thr	aaa Lys	tat Tyr	960
305					310					315					320	
cca Pro	gaa Glu	gag Glu	ata Ile	cca Pro	gac Asp	tat Tyr	ttc Phe	aaa Lys	caa Gln	gca Ala	ttt Phe	cct Pro	gaa Glu	ggc Gly	ctg Leu	1008
				325					330					335		
tca Ser	tgg Trp	gaa Glu	agg Arg	tcg Ser	ttg Leu	gag Glu	ttc Phe	gaa Glu	gat Asp	ggg Gly	ggg Gly	tcc Ser	gct Ala	tca Ser	gtc Val	1056
			340					345				350				
agt Ser	gcg Ala	cat His	ata Ile	agc Ser	ctt Leu	aga Arg	gga Gly	aac Asn	acc Thr	ttc Phe	tac Tyr	cac His	aaa Lys	tcc Ser	aaa Lys	1104
		355				360						365				
ttt Phe	act Thr	ggg Gly	gtt Val	aac Asn	ttt Phe	cct Pro	gcc Ala	gat Asp	ggg Gly	cct Pro	atc Ile	atg Met	caa Gln	aac Asn	caa Gln	1152
	370					375					380					
agt Ser	gtt Val	gat Asp	tgg Trp	gag Glu	cca Pro	tca Ser	acc Thr	gag Glu	aaa Lys	att Ile	act Thr	gcc Ala	agc Ser	gac Asp	gga Gly	1200
385					390					395					400	
gtt Val	ctg Leu	aag Lys	ggg Gly	gat Asp	gtt Val	acg Thr	atg Met	tac Tyr	cta Leu	aaa Lys	ctt Leu	gaa Glu	gga Gly	ggc Gly	ggc Gly	1248
			405						410				415			
aat Asn	cac His	aaa Lys	tgc Cys	caa Gln	ttc Phe	aag Lys	act Thr	act Thr	tac Tyr	aag Lys	gcg Ala	gca Ala	aaa Lys	aag Lys	att Ile	1296
			420				425					430				

ctt aaa atg cca gga agc cat tac atc agc cat cgc ctc gtc agg aaa 1344
 Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys
 435 440 445

acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1392
 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
 450 455 460

taa 1395

<210> 37

<211> 221

<212> PRT

<213> Montipora. sp

<400> 37

Met Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly
 1 5 10 15

Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys
 20 25 30

Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly
 35 40 45

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr Gly
 50 55 60

Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys
 65 70 75 80

Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met His Phe Glu
 85 90 95

Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn
 100 105 110

Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro Asn
 115 120 125

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu
 130 135 140

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala
 145 150 155 160

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr
 165 170 175

Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp
 180 185 190

Arg Lys Leu Asp Val Thr Ser His Asn Lys Asp Tyr Thr Phe Val Glu
 195 200 205

Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 38
 <211> 666
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(663)

<400> 38

atg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca ggc	48
Met Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly	
1 5 10 15	
acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag	96
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys	
20 25 30	
cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggt gga	144
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly	
35 40 45	
cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac gga	192
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr Gly	
50 55 60	
agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag	240
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys	
65 70 75 80	
cag tca ttc cct gag gga tat aca tgg gag agg atc atg cac ttt gaa	288
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met His Phe Glu	
85 90 95	
gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac	336
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn	
100 105 110	
tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc aat	384
Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro Asn	
115 120 125	
gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag	432
Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu	
130 135 140	
cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct	480
Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala	
145 150 155 160	
ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act	528
Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr	
165 170 175	

tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt gac 576
 Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp
 180 185 190

cgc aaa ctg gat gta acc agt cac aac aag gat tac aca ttt gtt gag 624
 Arg Lys Leu Asp Val Thr Ser His Asn Lys Asp Tyr Thr Phe Val Glu
 195 200 205

cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 666
 Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 39

<211> 222

<212> PRT

<213> Montipora. sp

<400> 39

Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
 1 5 10 15

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
 20 25 30

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
 35 40 45

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr
 50 55 60

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
 65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe
 85 90 95

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
 100 105 110

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro
 115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140

Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met
 145 150 155 160

Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175

Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val
 180 185 190

Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205

Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 40

<211> 669

<212> DNA

<213> Montipora. sp

<220>

<221> CDS

<222> (1)..(666)

<400> 40

atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca 48
 Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
 1 5 10 15

ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96
 Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
 20 25 30

aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144
 Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
 35 40 45

gga cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac 192
 Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr
 50 55 60

gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240
 Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
 65 70 75 80

aag cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttt 288
 Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe
 85 90 95

gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336
 Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
 100 105 110

aac tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc 384
 Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro
 115 120 125

aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140

gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat ttt atg 480
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met
 145 150 155 160

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gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct 528
Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
      165                      170                      175

act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt 576
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val
      180                      185                      190

gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
      195                      200                      205

gag cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 669
Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
      210                      215                      220

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<210> 41
<211> 222
<212> PRT
<213> Montipora. sp

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<400> 41
Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
  1           5           10           15

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
      20           25           30

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
      35           40           45

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr
      50           55           60

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
      65           70           75           80

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe
      85           90           95

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
      100          105          110

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro
      115          120          125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
      130          135          140

Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
      145          150          155          160

Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
      165          170          175

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Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile
 180 185 190

Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205

Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 42
 <211> 669
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(666)

<400> 42

atg	gtg	agt	gtg	atc	gct	aaa	caa	atg	acc	tac	aag	gtt	tat	atg	tca	48
Met	Val	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	Ser	
1				5				10					15			
ggc	acg	gtc	aat	gga	cac	tac	ttt	gag	gtc	gaa	ggc	gat	gga	aaa	gga	96
Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	Gly	
			20					25					30			
aag	cct	tac	gag	gga	gag	cag	aca	gta	aag	ctc	act	gtc	acc	aag	ggc	144
Lys	Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly	
			35				40					45				
gga	cct	ctg	cca	ttt	gct	tgg	gat	att	tta	tca	cca	ctg	ttt	cag	tac	192
Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Phe	Gln	Tyr	
	50					55					60					
gga	agc	ata	cca	ttc	acc	aag	tac	cct	gaa	gac	atc	cct	gat	tat	gta	240
Gly	Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val	
	65				70				75						80	
aag	cag	tca	ttc	cct	gag	gga	tat	aca	tgg	gag	agg	acc	atg	aac	ttt	288
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Met	Asn	Phe	
			85					90						95		
gaa	gat	ggt	gca	gtg	tgt	act	gtc	agc	aat	gat	tcc	agc	atc	caa	ggc	336
Glu	Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly	
			100					105					110			
aac	tgt	ttc	atc	tac	aat	gtc	aaa	atc	tct	ggt	acg	aac	ttt	cct	ccc	384
Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	Pro	
		115					120					125				
aat	gga	cct	gtt	atg	cag	aag	aag	aca	cag	ggc	tgg	gaa	ccc	agc	act	432
Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser	Thr	
	130					135					140					

gag	cgt	ctc	ttt	gca	cga	gat	gga	atg	ctg	ata	gga	aac	gat	tat	atg	480
Glu	Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr	Met	
145					150					155					160	
gct	ctg	aag	ttg	gaa	gga	ggt	ggt	cac	tat	ttg	tgt	gaa	ttt	aaa	tct	528
Ala	Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	Ser	
				165					170					175		
act	tac	aag	gca	aag	aag	cct	gtg	agg	atg	cca	ggg	tat	cac	tat	att	576
Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	Ile	
			180					185					190			
gac	cgc	aaa	ctg	gat	gta	acc	agt	cac	aac	agg	gat	tac	aca	tct	gtt	624
Asp	Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser	Val	
		195					200					205				
gag	cag	tgt	gaa	ata	gcc	att	gca	cgc	cac	tct	ttg	ctc	ggg	tga		669
Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly			
	210					215					220					

<210> 43
 <211> 222
 <212> PRT
 <213> Montipora. sp

<400> 43
 Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
 1 5 10 15

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
 20 25 30

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
 35 40 45

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Met Cys Tyr
 50 55 60

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
 65 70 75 80

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe
 85 90 95

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
 100 105 110

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro
 115 120 125

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140

Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
 145 150 155 160

Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175
 Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile
 180 185 190
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205
 Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 44
 <211> 669
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1) .. (666)

<400> 44

atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca	48
Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser	
1 5 10 15	
ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga	96
Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly	
20 25 30	
aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt	144
Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly	
35 40 45	
gga cct ctg cca ttt gct tgg gat att tta tca cca ctg atg tgt tac	192
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Met Cys Tyr	
50 55 60	
gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta	240
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val	
65 70 75 80	
aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac ttt	288
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe	
85 90 95	
gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc	336
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly	
100 105 110	
aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc	384
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro	
115 120 125	

aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140
 gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met
 145 150 155 160
 gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528
 Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175
 act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576
 Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile
 180 185 190
 gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205
 gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669
 Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 210 215 220

<210> 45
 <211> 255
 <212> PRT
 <213> Montipora. sp

<400> 45
 Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30
 Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45
 Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln
 85 90 95
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
 115 120 125
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140

Gly	Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Glu	Asn	Phe	Pro
145					150					155					160
Pro	Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser
				165					170					175	
Thr	Glu	Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr
			180					185					190		
Met	Ala	Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys
		195					200					205			
Ser	Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Arg	His	Glu
	210					215					220				
Ile	Asp	Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser
225					230					235					240
Val	Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly	
				245					250					255	

<210> 46
 <211> 765
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1) .. (765)

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Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Met	Ala	Ser	Met	Thr	
1				5					10					15		
ggt	gga	cag	caa	atg	ggt	cgg	gat	ctg	tac	gac	gat	gac	gat	aag	gat	96
Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	Asp	
			20					25					30			
ccc	atg	gtg	agt	gtg	atc	gct	aaa	caa	atg	acc	tac	aag	gtt	tat	atg	144
Pro	Met	Val	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	
		35					40					45				
tca	ggc	acg	gtc	aat	gga	cac	tac	ttt	gag	gtc	gaa	ggc	gat	gga	aaa	192
Ser	Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	
	50					55					60					
gga	aag	cct	tac	gag	gga	gag	cag	aca	gta	aag	ctc	act	gtc	acc	aag	240
Gly	Lys	Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	
65					70					75					80	
ggt	gga	cct	ctg	cca	ttt	gct	tgg	gat	att	tta	tca	cca	cag	ttc	cag	288
Gly	Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Gln	Phe	Gln	
				85					90						95	

tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110

 ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac 384
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
 115 120 125

 ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140

 ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct 480
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
 145 150 155 160

 ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
 165 170 175

 act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
 180 185 190

 atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624
 Met Ala Leu Lys Leu Glu Gly Gly His Tyr Leu Cys Glu Phe Lys
 195 200 205

 tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag 672
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
 210 215 220

 att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
 225 230 235 240

 gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 765
 Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 245 250 255

<210> 47

<211> 255

<212> PRT

<213> Montipora. sp

<400> 47

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45

Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60

Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln
 85 90 95
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
 115 120 125
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
 145 150 155 160
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
 165 170 175
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
 180 185 190
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
 195 200 205
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
 210 215 220
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
 225 230 235 240
 Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 245 250 255

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 <212> DNA
 <213> Montipora. sp

<220>
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 ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg	144
Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met	
35 40 45	
tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa	192
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys	
50 55 60	
gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag	240
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys	
65 70 75 80	
ggg gga cct ctg cca ttt gct tgg gat att tta tca cca cag ctt cag	288
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln	
85 90 95	
tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat	336
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr	
100 105 110	
ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac	384
Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn	
115 120 125	
ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa	432
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln	
130 135 140	
ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct	480
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro	
145 150 155 160	
ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc	528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser	
165 170 175	
act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat	576
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr	
180 185 190	
atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa	624
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys	
195 200 205	
tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag	672
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu	
210 215 220	
att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct	720
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser	
225 230 235 240	
gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt	765
Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly	
245 250 255	

<210> 49

<211> 747

<212> PRT

<213> Montipora. sp

<400> 49

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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
			35				40					45			
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75					80
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
				85					90					95	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
			115				120					125			
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155					160
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
				165					170					175	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
			180					185					190		
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
		195				200						205			
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210					215					220				
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
225					230					235					240
Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Val	Asp	Gly	Thr
				245					250					255	
Ala	Gly	Pro	Leu	Tyr	Asp	Glu	Val	Asp	Lys	Asp	Pro	Met	Ala	Ser	Ser
			260					265					270		

Glu	Asp	Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val	Arg	Met	Glu	Gly	
		275					280					285				
Ser	Val	Asn	Gly	His	Glu	Phe	Glu	Ile	Glu	Gly	Glu	Gly	Glu	Gly	Arg	
	290					295					300					
Pro	Tyr	Glu	Gly	Thr	Gln	Thr	Ala	Lys	Leu	Lys	Val	Thr	Lys	Gly	Gly	
305					310					315					320	
Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Gln	Phe	Gln	Tyr	Gly	
			325						330					335		
Ser	Lys	Ala	Tyr	Val	Lys	His	Pro	Ala	Asp	Ile	Pro	Asp	Tyr	Leu	Lys	
		340						345					350			
Leu	Ser	Phe	Pro	Glu	Gly	Phe	Lys	Trp	Glu	Arg	Val	Met	Asn	Phe	Glu	
		355					360					365				
Asp	Gly	Gly	Val	Val	Thr	Val	Thr	Gln	Asp	Ser	Ser	Leu	Gln	Asp	Gly	
	370					375					380					
Glu	Phe	Ile	Tyr	Lys	Val	Lys	Leu	Arg	Gly	Thr	Asn	Phe	Pro	Ser	Asp	
385					390					395					400	
Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Met	Gly	Trp	Glu	Ala	Ser	Thr	Glu	
				405					410					415		
Arg	Met	Tyr	Pro	Glu	Asp	Gly	Ala	Leu	Lys	Gly	Glu	Ile	Lys	Met	Arg	
		420						425					430			
Leu	Lys	Leu	Lys	Asp	Gly	Gly	His	Tyr	Asp	Ala	Glu	Val	Lys	Thr	Thr	
		435					440					445				
Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Ala	Tyr	Lys	Thr	Asp	
	450					455					460					
Ile	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr	Thr	Ile	Val	Glu	
465					470					475					480	
Gln	Tyr	Glu	Arg	Ala	Glu	Gly	Arg	His	Ser	Thr	Gly	Ala	Ser	Gly	Leu	
				485					490					495		
Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Val	Asp	Gly	Thr	Ala	Gly	
			500					505					510			
Pro	Leu	Tyr	Asp	Glu	Val	Gly	Lys	Asp	Pro	Met	Ala	Ser	Ser	Glu	Asp	
		515					520					525				
Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val	Arg	Met	Glu	Gly	Ser	Val	
	530					535					540					
Asn	Gly	His	Glu	Phe	Glu	Ile	Glu	Gly	Glu	Gly	Glu	Gly	Arg	Pro	Tyr	
545					550					555					560	
Glu	Gly	Thr	Gln	Thr	Ala	Lys	Leu	Lys	Val	Thr	Lys	Gly	Gly	Pro	Leu	
				565					570					575		

Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys
 580 585 590
 Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
 595 600 605
 Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly
 610 615 620
 Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe
 625 630 635 640
 Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro
 645 650 655
 Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met
 660 665 670
 Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys
 675 680 685
 Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
 690 695 700
 Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
 705 710 715 720
 Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr
 725 730 735
 Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
 740 745

<210> 50
 <211> 2241
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(2241)

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 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag	240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
gga ctc aga tct cga gct caa gct tcg aat tct gca gtc gac ggt acc	768
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr	
245 250 255	
gcg ggc ccg ctg tac gac gaa gtc gat aag gat ccg atg gcc tcc tcc	816
Ala Gly Pro Leu Tyr Asp Glu Val Asp Lys Asp Pro Met Ala Ser Ser	
260 265 270	

gag	gac	gtc	atc	aag	gag	ttc	atg	cgc	ttc	aag	gtg	cgc	atg	gag	ggc	864
Glu	Asp	Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val	Arg	Met	Glu	Gly	
		275					280					285				
tcc	gtg	aac	ggc	cac	gag	ttc	gag	atc	gag	ggc	gag	ggc	gag	ggc	cgc	912
Ser	Val	Asn	Gly	His	Glu	Phe	Glu	Ile	Glu	Gly	Glu	Gly	Glu	Gly	Arg	
	290					295					300					
ccc	tac	gag	ggc	acc	cag	acc	gcc	aag	ctg	aag	gtg	acc	aag	ggc	ggc	960
Pro	Tyr	Glu	Gly	Thr	Gln	Thr	Ala	Lys	Leu	Lys	Val	Thr	Lys	Gly	Gly	
305					310					315					320	
ccc	ctg	ccc	ttc	gcc	tgg	gac	atc	ctg	tcc	cct	cag	ttc	cag	tac	ggc	1008
Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Gln	Phe	Gln	Tyr	Gly	
				325					330					335		
tcc	aag	gcc	tac	gtg	aag	cac	ccc	gcc	gac	atc	ccc	gac	tac	ttg	aag	1056
Ser	Lys	Ala	Tyr	Val	Lys	His	Pro	Ala	Asp	Ile	Pro	Asp	Tyr	Leu	Lys	
			340					345					350			
ctg	tcc	ttc	ccc	gag	ggc	ttc	aag	tgg	gag	cgc	gtg	atg	aac	ttc	gag	1104
Leu	Ser	Phe	Pro	Glu	Gly	Phe	Lys	Trp	Glu	Arg	Val	Met	Asn	Phe	Glu	
		355					360					365				
gac	ggc	ggc	gtg	gtg	acc	gtg	acc	cag	gac	tcc	tcc	ctg	cag	gac	ggc	1152
Asp	Gly	Gly	Val	Val	Thr	Val	Thr	Gln	Asp	Ser	Ser	Leu	Gln	Asp	Gly	
	370					375					380					
gag	ttc	atc	tac	aag	gtg	aag	ctg	cgc	ggc	acc	aac	ttc	ccc	tcc	gac	1200
Glu	Phe	Ile	Tyr	Lys	Val	Lys	Leu	Arg	Gly	Thr	Asn	Phe	Pro	Ser	Asp	
385					390					395					400	
ggc	ccc	gta	atg	cag	aag	aag	acc	atg	ggc	tgg	gag	gcc	tcc	acc	gag	1248
Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Met	Gly	Trp	Glu	Ala	Ser	Thr	Glu	
				405					410					415		
cgg	atg	tac	ccc	gag	gac	ggc	gcc	ctg	aag	ggc	gag	atc	aag	atg	agg	1296
Arg	Met	Tyr	Pro	Glu	Asp	Gly	Ala	Leu	Lys	Gly	Glu	Ile	Lys	Met	Arg	
			420					425					430			
ctg	aag	ctg	aag	gac	ggc	ggc	cac	tac	gac	gcc	gag	gtc	aag	acc	acc	1344
Leu	Lys	Leu	Lys	Asp	Gly	Gly	His	Tyr	Asp	Ala	Glu	Val	Lys	Thr	Thr	
		435					440					445				
tac	atg	gcc	aag	aag	ccc	gtg	cag	ctg	ccc	ggc	gcc	tac	aag	acc	gac	1392
Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Ala	Tyr	Lys	Thr	Asp	
	450					455					460					
atc	aag	ctg	gac	atc	acc	tcc	cac	aac	gag	gac	tac	acc	atc	gtg	gaa	1440
Ile	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr	Thr	Ile	Val	Glu	
465					470					475					480	
cag	tac	gag	cgc	gcc	gag	ggc	cgc	cac	tcc	acc	ggc	gcc	tcc	gga	ctc	1488
Gln	Tyr	Glu	Arg	Ala	Glu	Gly	Arg	His	Ser	Thr	Gly	Ala	Ser	Gly	Leu	
				485					490					495		

aga tct cga gct caa gct tcg aat tct gca gtc gac ggt acc gcg ggc	1536
Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly	
500 505 510	
ccg ctg tac gac gaa gtc ggt aag gat ccg atg gcc tcc tcc gag gac	1584
Pro Leu Tyr Asp Glu Val Gly Lys Asp Pro Met Ala Ser Ser Glu Asp	
515 520 525	
gtc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc tcc gtg	1632
Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly Ser Val	
530 535 540	
aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc ccc tac	1680
Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr	
545 550 555 560	
gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg	1728
Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu	
565 570 575	
ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc tcc aag	1776
Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys	
580 585 590	
gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag ctg tcc	1824
Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser	
595 600 605	
ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc	1872
Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly	
610 615 620	
ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc	1920
Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe	
625 630 635 640	
atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc	1968
Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro	
645 650 655	
gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg	2016
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met	
660 665 670	
tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag	2064
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys	
675 680 685	
ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg	2112
Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met	
690 695 700	
gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag	2160
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys	
705 710 715 720	

ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac 2208
 Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr
 725 730 735

gag cgc gcc gag ggc cgc cac tcc acc ggc gcc 2241
 Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
 740 745

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 Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 35 40 45
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 50 55 60
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 65 70 75 80
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 85 90 95
 Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 100 105 110
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 115 120 125
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 130 135 140
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 145 150 155 160
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 165 170 175
 Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 180 185 190
 Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 195 200 205
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 210 215 220

Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	225	230	235	240
Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	245	250	255	
Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	260	265	270	
Ser	Ser	Ser	Glu	Leu	Ser	Gly	Asp	Glu	Val	Asp	Gly	Thr	Met	Val	Ser	275	280	285	
Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	Ser	Gly	Thr	Val	290	295	300	
Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	Gly	Lys	Pro	Tyr	305	310	315	320
Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly	Gly	Pro	Leu	325	330	335	
Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Phe	Gln	Tyr	Gly	Ser	Ile	340	345	350	
Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val	Lys	Gln	Ser	355	360	365	
Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Met	Asn	Phe	Glu	Asp	Gly	370	375	380	
Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly	Asn	Cys	Phe	385	390	395	400
Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	Pro	Asn	Gly	Pro	405	410	415	
Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser	Thr	Glu	Arg	Leu	420	425	430	
Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr	Met	Ala	Leu	Lys	435	440	445	
Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	Ser	Thr	Tyr	Lys	450	455	460	
Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	Ile	Asp	Arg	Lys	465	470	475	480
Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser	Val	Glu	Gln	Cys	485	490	495	
Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly						500	505		

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<220>
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<400> 52

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ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat	96
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp	
20 25 30	
ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc	144
Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile	
35 40 45	
ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc	192
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser	
50 55 60	
ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc	240
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe	
65 70 75 80	
atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc	288
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr	
85 90 95	
acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg	336
Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met	
100 105 110	
aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag	384
Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln	
115 120 125	
gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc	432
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala	
130 135 140	
gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag	480
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys	
145 150 155 160	
ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag	528
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu	
165 170 175	
tac aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag	576
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
180 185 190	

aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc	624
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly	
195 200 205	
agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	672
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
210 215 220	
ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc	720
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala	
225 230 235 240	
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	768
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
245 250 255	
ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	816
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
260 265 270	
tcc tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agt	864
Ser Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser	
275 280 285	
gtg atc gct aaa caa atg acc tac aag gtt tat atg tca ggc acg gtc	912
Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val	
290 295 300	
aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct tac	960
Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr	
305 310 315 320	
gag gga gag cag aca gta aag ctc act gtc acc aag ggt gga cct ctg	1008
Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro Leu	
325 330 335	
cca ttt gct tgg gat att tta tca cca ctg ttt cag tac gga agc ata	1056
Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr Gly Ser Ile	
340 345 350	
cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag cag tca	1104
Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser	
355 360 365	
ttc cct gag gga tat aca tgg gag agg acc atg aac ttt gaa gat ggt	1152
Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe Glu Asp Gly	
370 375 380	
gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt ttc	1200
Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe	
385 390 395 400	
atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc aat gga cct	1248
Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro Asn Gly Pro	
405 410 415	

gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act gag cgt ctc 1296
 Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr Glu Arg Leu
 420 425 430
 ttt gca cga gat gga atg ctg ata gga aac gat tat atg gct ctg aag 1344
 Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met Ala Leu Lys
 435 440 445
 ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct act tac aag 1392
 Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys
 450 455 460
 gca aag aag cct gtg agg atg cca ggg tat cac tat att gac cgc aaa 1440
 Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile Asp Arg Lys
 465 470 475 480
 ctg gat gta acc agt cac aac agg gat tac aca tct gtt gag cag tgt 1488
 Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val Glu Gln Cys
 485 490 495
 gaa ata gcc att gca cgc cac tct ttg ctc ggt 1521
 Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 500 505

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 <212> PRT
 <213> Montipora. sp

<400> 53
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 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30
 Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45
 Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln
 85 90 95
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn
 115 120 125
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140

Gly	Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	145	150	155	160
Pro	Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser	165	170	175	
Thr	Glu	Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr	180	185	190	
Met	Ala	Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	195	200	205	
Ser	Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	210	215	220	
Ile	Asp	Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser	225	230	235	240
Val	Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly	Ser	245	250	255	
Ser	Ser	Glu	Leu	Ser	Gly	Asp	Glu	Val	Asp	Gly	Thr	Met	Val	Ser	Lys	260	265	270	
Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	275	280	285	
Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	290	295	300	
Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	305	310	315	320
Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Trp	Gly	325	330	335	
Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	340	345	350	
Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	355	360	365	
Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	370	375	380	
Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	385	390	395	400
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser	405	410	415	
His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala	420	425	430	
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	435	440	445	

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 450 455 460

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 465 470 475 480

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 485 490 495

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 500 505

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 <211> 1521
 <212> DNA
 <213> Montipora. sp

<220>
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ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144
 Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45

tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192
 Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60

gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80

ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt cag 288
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln
 85 90 95

tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110

gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac 384
 Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn
 115 120 125

ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa	432
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln	
130 135 140	
ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct	480
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro	
145 150 155 160	
ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc	528
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser	
165 170 175	
act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat	576
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr	
180 185 190	
atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa	624
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys	
195 200 205	
tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat	672
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr	
210 215 220	
att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct	720
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser	
225 230 235 240	
gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tcc	768
Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly Ser	
245 250 255	
tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agc aag	816
Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser Lys	
260 265 270	
ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac	864
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp	
275 280 285	
ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc	912
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly	
290 295 300	
gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc	960
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly	
305 310 315 320	
aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc	1008
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly	
325 330 335	
gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc	1056
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe	
340 345 350	

ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc 1104
 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 355 360 365

 ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag 1152
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 370 375 380

 ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 1200
 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 385 390 395 400

 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 1248
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
 405 410 415

 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 1296
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
 420 425 430

 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 1344
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 435 440 445

 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 1392
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 450 455 460

 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 1440
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 465 470 , 475 480

 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 1488
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 485 490 495

 ggg atc act ctc ggc atg gac gag ctg tac aag 1521
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 500 505

<210> 55

<211> 411

<212> PRT

<213> Montipora. sp

<400> 55

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 35 40 45

Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser		
50						55					60						
Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe		
65					70					75					80		
Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr		
				85					90					95			
Thr	Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met		
			100					105					110				
Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln		
		115					120					125					
Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala		
130						135					140						
Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys		
145					150					155					160		
Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu		
				165					170					175			
Tyr	Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys		
			180					185					190				
Asn	Gly	Ile	Lys	Ala	His	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly		
		195					200					205					
Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
	210					215					220						
Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala		
225					230					235					240		
Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu		
				245					250					255			
Phe	Val	Thr	Ala	Ala	Arg	Met	His	Asp	Gln	Leu	Thr	Glu	Glu	Gln	Ile		
			260					265					270				
Ala	Glu	Phe	Lys	Glu	Ala	Phe	Ser	Leu	Phe	Asp	Lys	Asp	Gly	Asp	Gly		
		275					280					285					
Thr	Ile	Thr	Thr	Lys	Glu	Leu	Gly	Thr	Val	Met	Arg	Ser	Leu	Gly	Gln		
	290					295					300						
Asn	Pro	Thr	Glu	Ala	Glu	Leu	Gln	Asp	Met	Ile	Asn	Glu	Val	Asp	Ala		
305					310					315					320		
Asp	Gly	Asn	Gly	Thr	Ile	Tyr	Phe	Pro	Glu	Phe	Leu	Thr	Met	Met	Ala		
				325					330					335			
Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu	Glu	Glu	Ile	Arg	Glu	Ala	Phe		
			340					345					350				

Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu
 355 360 365

Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val
 370 375 380

Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Asp Gly Gln Val Asn
 385 390 395 400

Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys
 405 410

<210> 56
 <211> 1233
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(1233)

<400> 56

atg	cgg	ggt	tct	cat	cat	cat	cat	cat	cat	ggt	atg	gct	agc	atg	act	48
Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Met	Ala	Ser	Met	Thr	
1				5					10					15		
ggt	gga	cag	caa	atg	ggt	cgg	gat	ctg	tac	gac	gat	gac	gat	aag	gat	96
Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	Asp	
			20					25						30		
ccc	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	144
Pro	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	
		35						40					45			
ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	agg	ttc	agc	gtg	tcc	192
Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser	
	50					55					60					
ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	240
Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	
65					70					75					80	
atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	288
Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	
				85					90					95		
acc	ctg	acc	tgg	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	336
Thr	Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	
			100					105					110			
aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	384
Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	
		115					120					125				

gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	432
Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	
130						135					140					
gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	480
Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	
145					150					155					160	
ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	528
Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	
				165					170					175		
tac	aac	tat	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	576
Tyr	Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	
			180					185					190			
aac	ggc	atc	aag	gcc	cac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	624
Asn	Gly	Ile	Lys	Ala	His	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	
		195					200					205				
agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	672
Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	
	210					215					220					
ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	720
Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	
225					230					235					240	
ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	768
Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	
				245					250					255		
ttc	gtg	acc	gcc	gcc	cgc	atg	cat	gac	caa	ctg	aca	gaa	gag	cag	att	816
Phe	Val	Thr	Ala	Ala	Arg	Met	His	Asp	Gln	Leu	Thr	Glu	Glu	Gln	Ile	
			260					265					270			
gca	gag	ttc	aaa	gaa	gcc	ttc	tca	tta	ttc	gac	aag	gat	ggg	gac	ggc	864
Ala	Glu	Phe	Lys	Glu	Ala	Phe	Ser	Leu	Phe	Asp	Lys	Asp	Gly	Asp	Gly	
		275					280					285				
acc	atc	acc	aca	aag	gaa	ctt	ggc	acc	gtt	atg	agg	tcg	ctt	gga	caa	912
Thr	Ile	Thr	Thr	Lys	Glu	Leu	Gly	Thr	Val	Met	Arg	Ser	Leu	Gly	Gln	
	290					295					300					
aac	cca	acg	gaa	gca	gaa	ttg	cag	gat	atg	atc	aat	gaa	gtc	gat	gct	960
Asn	Pro	Thr	Glu	Ala	Glu	Leu	Gln	Asp	Met	Ile	Asn	Glu	Val	Asp	Ala	
305					310					315					320	
gat	ggc	aat	gga	acg	att	tac	ttt	cct	gaa	ttt	ctt	act	atg	atg	gct	1008
Asp	Gly	Asn	Gly	Thr	Ile	Tyr	Phe	Pro	Glu	Phe	Leu	Thr	Met	Met	Ala	
				325					330					335		
aga	aaa	atg	aag	gac	aca	gac	agc	gaa	gag	gaa	atc	cga	gaa	gca	ttc	1056
Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu	Glu	Glu	Ile	Arg	Glu	Ala	Phe	
			340					345					350			

cgt gtt ttt gac aag gat ggg aac ggc tac atc agc gct gct gaa tta	1104
Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu	
355 360 365	
cgt cac gtc atg aca aac ctc ggg gag aag tta aca gat gaa gaa gtt	1152
Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val	
370 375 380	
gat gaa atg ata agg gaa gca gat atc gat ggt gat ggc caa gta aac	1200
Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Asp Gly Gln Val Asn	
385 390 395 400	
tat gaa gag ttt gta caa atg atg aca gca aag	1233
Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys	
405 410	

<210> 57
 <211> 288
 <212> PRT
 <213> Montipora. sp

<400> 57	
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr	
1 5 10 15	
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp	
20 25 30	
Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn	
35 40 45	
Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Gly Ser	
50 55 60	
Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr	
65 70 75 80	
Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly	
85 90 95	
Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr	
100 105 110	
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe	
115 120 125	
Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp	
130 135 140	
Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met	
145 150 155 160	
Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile	
165 170 175	

Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe
 180 185 190

Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro
 195 200 205

Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp
 210 215 220

Tyr Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe
 225 230 235 240

Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His
 245 250 255

Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr
 260 265 270

Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 275 280 285

<210> 58
 <211> 864
 <212> DNA
 <213> Montipora. sp

<220>
 <221> CDS
 <222> (1)..(864)

<400> 58
 atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48
 Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15

ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

ccc aag agg cgc tgg aag aaa aac ttc att gcc gtc agc gct gcc aac 144
 Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn
 35 40 45

cgg ttc aag aag atc tcc agc tcc ggg gca ctg gga ggt gga ggt agt 192
 Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Gly Ser
 50 55 60

gag ctc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat 240
 Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr
 65 70 75 80

atg tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga 288
 Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly
 85 90 95

aaa gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc	336
Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr	
100 105 110	
aag ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt	384
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe	
115 120 125	
cag tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat	432
Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp	
130 135 140	
tat gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg	480
Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met	
145 150 155 160	
aac ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc	528
Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile	
165 170 175	
caa ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt	576
Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe	
180 185 190	
cct ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc	624
Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro	
195 200 205	
agc act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat	672
Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp	
210 215 220	
tat atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt	720
Tyr Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe	
225 230 235 240	
aaa tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac	768
Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His	
245 250 255	
tat att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca	816
Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr	
260 265 270	
tct gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt	864
Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly	
275 280 285	

<210> 59

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 59
ccagagatga agatgaggta ctacatggac ggc 33

<210> 60
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 60
catgagttca caattgaagg tgaaggc 27

<210> 61
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 61
gaaggcacag gcagacctta cgaggga 27

<210> 62
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 62
ccaatgcctt tcgcgtttga cttagtg 27

<210> 63
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 63
ttagtgtcac acgtgttctg ttacggc 27

<210> 64
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 64
gaaaggtcgt tggagttcga agatggt

27

<210> 65
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 65
gaagatggtg ggtccgcttc agtcagtgcg

30

<210> 66
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 66
agccttagag gaaacacctt ctaccacaaa tcca

34

<210> 67
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 67
caaatccaaa ttactgggg ttaactttcc tg

32

<210> 68
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 68
 gccgatgggc ctatcatgca aaaccaaagt 30

 <210> 69
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 69
 gccgatgggc ctatcatgca aaaccaaagt gttgattggg agcca 45

 <210> 70
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 70
 gagaaaatta ctgccagcga cggagttctg aag 33

 <210> 71
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 71
 gatgttacga tgtacctaaa acttgaagga ggcggcaatc ac 42

 <210> 72
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 72
 cttaaaatgc caggaagcca ttacatcagc catcgctcg tcagg 45

<210> 73
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 73
 gatgcagtag ctcatccct cgagcaccac cacc 34

<210> 74
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 74
 gaaggrtgyg tcaayggrca y 21

<210> 75
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 75
 acvggdccat ydgvaagaaa rtt 23

<210> 76
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<220>
 <221> modified_base
 <222> (24)..(25)
 <223> inosine

<220>
<221> modified_base
<222> (29)..(30)
<223> inosine

<220>
<221> modified_base
<222> (34)..(35)
<223> inosine

<400> 76
ggccacgcgt cgactagtagt gggnnngggnn gggnnng

36

<210> 77
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 77
ctcaggaat gactgcttta cat

23

<210> 78
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 78
ggccacgcgt cgactagtagt

20

<210> 79
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 79
gtcttcaggg tacttggtga

20

<210> 80
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 80
 atgtaaagca gtcattccct gag

23

<210> 81
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 81
 cccggatccg accatggcta ccttggttaa aga

33

<210> 82
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 82
 Asp Glu Val Asp
 1

<210> 83
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 83
 Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys
 1 5 10

<210> 84
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 84

Gly	Gly	Ser	Gly	Gly	Asp	Glu	Val	Asp	Gly	Thr	Gly	Gly	Ser
1				5					10				